parasites can easily be missed or barely noticeable so that their identification can be quite difficult. In such instances, videodermatoscopy might lead to the diagnosis and should be considered as a useful diagnostic aid. Image storage and sharing can also facilitate collaboration with experts and can enable timely recognition of unusual parasitic disorders imported from different geographic areas or tropical countries.

The cost of the equipment varies according to resolution quality, magnification capability, and image storage facility; costs range from 500 (for simple systems) to 10,000 (for sophisticated systems) euros. The expense is greatly outweighed by the advantages of avoiding the high cost of managing outbreaks of epidemic parasitoses resulting from misdiagnosis, treatment failures, and incomplete posttreatment monitoring (10).

Videodermatoscopy is a noninvasive way to diagnose some pruritic disorders while avoiding unnecessary, uncomfortable, and sometimes expensive investigations and treatments. Physicians without access to such equipment should consider promptly referring patients to the nearest available videodermatoscopy service for effective management.

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Distinguishing Nontuberculous Mycobacteria from Multidrug-Resistant Mycobacterium tuberculosis, China

To the Editor: Mycobacteria are commonly characterized by positive acid-fast staining. Most mycobacterial species belong to the nontuberculous mycobacteria (NTM), excluding species in the Mycobacterium tuberculosis complex and M. leprae. Both M. tuberculosis and NTM can induce pulmonary infection with similar symptoms and pulmonary radiographic findings (1). These similarities have led to difficulty in distinguishing these infections clinically.

As in many developing countries, the acid-fast stain is the only bacteriologic basis for diagnosing tuberculosis (TB) in primary health care institutions in China, where facilities are limited for M. tuberculosis culture, strain identification, and drug resistance detection. Thus, NTM is easily misdiagnosed as M. tuberculosis, and multidrug-resistant (MDR) TB is unable to be accurately identified. Patients with misdiagnosed TB usually are treated with the standard anti-TB regimens recommended by the Chinese government (i.e., 2HRZE/4HR [2 months of isoniazid (INH), rifampin (RIF), pyrazinamide, and ethambutol, followed by 4 months of INH and RIF 1 time daily] and 2HRZE/4HR, [2 months of INH, RIF, pyrazinamide, and ethambutol followed by 4 months of INH and RIF 3 times weekly]) (2), which often results in treatment failures. Misdiagnosis is a key hurdle for effective prevention and treatment of TB (3–5). To evaluate the effect of misdiagnosis on TB prevention, we determined the proportion of patients with MDR TB and NTM infection in primary health care institutions in Zhejiang Province, China.
findings would be useful for improving TB prevention and treatment.

During 2011–2012, sputum samples from 13,882 patients suspected of having TB in 8 counties in Zhejiang Province were used to culture mycobacteria. Each sample was seeded onto 2 pieces of Löwenstein-Jensen medium. A total of 1,410 samples grew mycobacteria confirmed as acid-fast bacilli by using Ziehl-Neelsen staining. The 1,410 samples were further identified by using the Mycobacteria Identification Array Kit (CapitalBio, Beijing, China). The kit contains 17 types of bacilli-specific 16S rRNA probes (i.e., M. tuberculosis complex, M. avium, M. intracellulare, M. gilvum, M. xenopi, M. smegmatis, M. aurum, M. terrae, M. gordoniae, M. chelonae/abscessus, M. phlei, M. scrofulaceum, M. fortuitum, M. szulga, M. ulcerans, M. marinum, and M. kansasii). With this method, M. tuberculosis and NTM can be distinguished, and the species of NTM can be identified (6–8). Of 1,410 positive strains, we identified 1,332 (94.5%) as M. tuberculosis and 78 (5.5%) as NTM. NTM strains were further identified as follows: M. intracellulare, 39 isolates; M. chelonae/abscessus, 12 isolates, M. kansasii, 13 isolates; M. avium, 3 isolates; M. fortuitum, 4 isolates; and M. scrofulaceum and M. szulga, 1 isolate each. For 5 isolates, strain could not be classified.

We detected drug resistance of 1,332 M. tuberculosis strains using a Tuberculosis Drug Resistance Detection Array Kit (CapitalBio) (9). The mutant points for RIF resistance were identified as follows: rpoB/C531G, C531T, CG531AC, A526C, A526G, A526T, C526A, C526G, C526T, T533C, A516G, A516T, G516T, T511C, T511G, C513A, A513T, and C522T (Table). Moreover, the kit contained 5 mutant points for INH resistance, including katG (G315A, G315C, G315T, and C315) and inhA (C-15T) (Table). Of 1,332 M. tuberculosis strains, we identified 1,115 (83.7%) RIF/INH-sensitive strains, 83 (6.2%) INH-resistant strains, and 47 (3.5%) RIF-resistant strains. Of the 1,410 positive strains, 88 (6.2%) were MDR tuberculosis strains.

The epidemiology of TB in Zhejiang Province reflects the situation in China and some developing countries (10). The clinical diagnosis and treatment of >80% TB cases in China are performed mainly by primary health care institutions. However, almost 80% of these medical institutions do not have the capability to culture M. tuberculosis, detect drug resistance, and identify strains (7). Of 1,410 strains obtained from the patients in 8 counties of Zhejiang Province, 218 (15.5%) were MDR TB, INH resistant, and RIF resistant. These affected patients could not be effectively treated with the national standard regimens. Specifically, 88 patients with MDR TB would be at risk for extensively drug-resistant TB, and 83 patients with INH-resistant TB and 47 with RIF-resistant TB would be at risk for MDR TB. In addition, we identified 78 (5.5%) NTM strains. With the acid-fast stain, these illnesses would be misidentified as TB and, in most instances, also would be reported as treatment failures. Clearly, accurate diagnosis provided by the technologies used in this study for distinguishing NTM and M. tuberculosis, Mycobacterium strain identification, and drug-resistance detection would increase the cure rate and effectively prevent TB epidemics.

For INH resistance, katG315 was a main mutant point in the M. tuberculosis strain; 140 (81.4%) of the 172 INH-resistant mutations were related to katG315. For RIF resistance, rpoB531 was a main mutant point; 84 (60.0%) of 140 RIF-resistant mutations were associated with rpoB531. Therefore, in future studies, more attention should be paid to the molecular epidemiology of katG315 and rpoB531.

In conclusion, using the techniques for M. tuberculosis culture, Mycobacterium strain identification, and drug-resistance detection is necessary. It should be urgently pursued for accurate TB diagnosis in primary health care institutions in China to improve the prevention, treatment, and control of TB.

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<table>
<thead>
<tr>
<th>Drug</th>
<th>Mutant times (mutant times of sites related to drug resistance)</th>
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<tbody>
<tr>
<td><strong>Isoniazid</strong></td>
<td></td>
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<tr>
<td>inhA-15 (C→T)</td>
<td>Mutant times for single site, no. (%)†</td>
</tr>
<tr>
<td>katG315 (G→C), (G→A)</td>
<td>32 (18.6)</td>
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<tr>
<td></td>
<td>140 (81.4)</td>
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<tr>
<td><strong>Rifampin</strong></td>
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<tr>
<td>rpoB511 (T→C)</td>
<td>Mutant times for single site, no. (%)†</td>
</tr>
<tr>
<td></td>
<td>140‡</td>
</tr>
<tr>
<td>rpoB513 (A→G)</td>
<td>10 (7.1)</td>
</tr>
<tr>
<td>rpoB516 (A→T), (A→G), (G→T)</td>
<td>2 (1.4)</td>
</tr>
<tr>
<td>rpoB526 (A→G), (A→T), (C→G), (G→T)</td>
<td>19 (13.6)</td>
</tr>
<tr>
<td></td>
<td>21 (15)</td>
</tr>
<tr>
<td>rpoB531 (C→G), (C→T)</td>
<td>84 (60.0)</td>
</tr>
<tr>
<td>rpoB533 (T→C)</td>
<td>4 (2.9)</td>
</tr>
</tbody>
</table>

*No. mutant times for single site/total no. mutant times of sites related to drug resistance.
†A strain simultaneously had katG315 (G→C) and inhA-15 (C→T).
‡Five strains had the double mutation of rpoB.
Schmallenberg Virus Circulation in High Mountain Ecosystem, Spain

To the Editor: Schmallenberg vi-

Mrs. D. Babić
Chairwoman
World Health Organization
Regional Office for Europe
Belgrade, Serbia

Dear Sirs,

We have read with great interest the recent communication by Dr. Kafani et al. (1) on the occurrence of Schmallenberg virus (SBV) in cattle in Serbia, as well as the surveillance of SBV within the WB-10 project (2), the European Reference Laboratory for Emergencies and Import Hazards, which we have been involved in recently.

We wish to provide further information about the SBV circulation in the Balkan Peninsula. Our previous studies (3,4) have shown that SBV has been circulating in the region since 2010, with outbreaks reported in cattle and sheep across the Balkan Peninsula, including Serbia, Montenegro, and Bosnia and Herzegovina. These outbreaks have been associated with the presence of SBV in the vector Culicoides midges, which are known to be vectors of this virus.

Furthermore, our studies have also shown that SBV has been detected in other vectors, such as Culicoides species, in the region. This suggests that SBV has the potential to be transmitted to other species of Culicoides midges, which could increase the risk of infection in susceptible livestock populations.

We therefore recommend that further studies be conducted to investigate the epidemiology of SBV in the Balkan Peninsula, and to assess the potential risk of transmission to other livestock populations.

Sincerely yours,

[Signature]

[Name]

[Position]

[Institution]